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☐	L4	L2 same background	76
☐	L3	l1 same backgrtound	0
☐	L2	microarray same noise	169
☐	L1	microarray same (noise or heterogenous or outlier or spurious)	205

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                     present
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NEWS  5  SEP 29      DISSABS now available on STN
NEWS  6  OCT 10      PCTFULL: Two new display fields added
NEWS  7  OCT 21      BIOSIS file reloaded and enhanced
NEWS  8  OCT 28      BIOSIS file segment of TOXCENTER reloaded and enhanced
NEWS  9  NOV 24      MSDS-CCOHS file reloaded
NEWS 10  DEC 08      CABA reloaded with left truncation
NEWS 11  DEC 08      IMS file names changed
NEWS 12  DEC 09      Experimental property data collected by CAS now available
                     in REGISTRY
NEWS 13  DEC 09      STN Entry Date available for display in REGISTRY and CA/CAplus
NEWS 14  DEC 17      DGENE: Two new display fields added
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NEWS 16  DEC 19      CROPU no longer updated; subscriber discount no longer
                     available
NEWS 17  DEC 22      Additional INPI reactions and pre-1907 documents added to CAS
                     databases
NEWS 18  DEC 22      IFIPAT/IFIUDB/IFICDB reloaded with new data and search fields
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              MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
              AND CURRENT DISCOVER FILE IS DATED 23 SEPTEMBER 2003
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FILE 'BIOSIS' ENTERED AT 13:52:27 ON 25 JAN 2004
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L1 1593 ARRAY AND (HETEROGENOUS OR NOISE OR OUTLIER OR SPURIOUS)

=> s l1 and microarray
L2 129 L1 AND MICROARRAY

=> s l2 and (nucleic acid or polynucleotide or probe)
L3 35 L2 AND (NUCLEIC ACID OR POLYNUCLEOTIDE OR PROBE)

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=> d 1-29 bib ab

L4 ANSWER 1 OF 29 MEDLINE on STN
Full Text
AN 2003356013 MEDLINE
DN 22770806 PubMed ID: 12888502
TI **Spurious** spatial periodicity of co-expression in **microarray** data due to printing design.
AU Balazsi Gabor; Kay Krin A; Barabasi Albert-Laszlo; Oltvai Zoltan N
CS Department of Pathology, Feinberg School of Medicine, Northwestern University, Ward Building 6-204, 303 East Chicago Avenue, Chicago, IL 60611, USA. g-balazsi@northwestern.edu. <g-balazsi@northwestern.edu>
SO NUCLEIC ACIDS RESEARCH, (2003 Aug 1) 31 (15) 4425-33.
Journal code: 0411011. ISSN: 1362-4962.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200308
ED Entered STN: 20030731
Last Updated on STN: 20030821
Entered Medline: 20030820
AB Global transcriptome data is increasingly combined with sophisticated mathematical analyses to extract information about the functional state of a cell. Yet the extent to which the results reflect experimental bias at the expense of true biological information remains largely unknown. Here we show that the spatial arrangement of **probes** on **microarrays** and the particulars of the printing procedure significantly affect the log-ratio data of mRNA expression levels measured during the Saccharomyces cerevisiae cell cycle. We present a numerical method that filters out these technology-derived contributions from the existing transcriptome data, leading to improved functional predictions. The example presented here underlines the need to routinely search and compensate for inherent experimental bias when analyzing systematically collected, internally consistent biological data sets.

L4 ANSWER 2 OF 29 MEDLINE on STN
Full Text
AN 2003554450 IN-PROCESS
DN PubMed ID: 14632467
TI ChipCheck--a program predicting total hybridization equilibria for DNA binding to small oligonucleotide **microarrays**.
AU Siegmund Karsten H; Steiner Ulrich E; Richert Clemens
CS Institute for Organic Chemistry, University of Karlsruhe (TH), D-76128 Karlsruhe, Germany.
SO Journal of chemical information and computer sciences, (2003 Nov-Dec) 43 (6) 2153-62.
Journal code: 7505012. ISSN: 0095-2338.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20031125
Last Updated on STN: 20031217
AB Presented here is the program ChipCheck that allows the computation of total hybridization equilibria for hybridization experiments involving small oligonucleotide **arrays**. The calculation requires the free energies of binding for all pairs of **probes** and targets as well as total strand concentrations and **probe** molecule numbers. ChipCheck has been tested computationally on **microarrays** with up to 100 spots and 42 target strands (4200 binding equilibria). It arrives at solutions through iterations employing the multidimensional Newton method. While currently running in simulation mode only, an extension of the approach to the exhaustive analysis of chip results is being outlined and may be implemented in the future. The output displays the extent of correct and cross hybridization both graphically and numerically. In principle, calculating total hybridization equilibria allows for eliminating **noise** from DNA chip results and thus an improvement in sensitivity and accuracy.

L4 ANSWER 3 OF 29 MEDLINE on STN
Full Text
AN 2003415080 MEDLINE
DN 22835105 PubMed ID: 12809552
TI Synergistic effects of epoxy- and amine-silanes on **microarray** DNA immobilization and hybridization.
AU Chiu Sung-Kay; Hsu Mandy; Ku Wei-Chi; Tu Ching-Yu; Tseng Yu-Tien; Lau Wai-Kwan; Yan Rong-Yih; Ma Jing-Tyan; Tzeng Chi-Meng
CS Department of Research and Development, U-Vision Biotech Inc., 3F No.132 Lane 235 Pao-Chiao Rd, Hsin-Tien City 231, Taipei, Taiwan.
SO BIOCHEMICAL JOURNAL, (2003 Sep 15) 374 (Pt 3) 625-32.
Journal code: 2984726R. ISSN: 1470-8728.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200309
ED Entered STN: 20030905
Last Updated on STN: 20031001
Entered Medline: 20030930
AB Most **microarray** slides are manufactured or coated with a layer of poly(L-lysine) or with silanes with different chemical functional groups, for the attachment of **nucleic acids** on to their surfaces. The efficiency with which **nucleic acids** bind to these surfaces is not high, because they can be washed away, especially in the case of spotting oligonucleotides. In view of this, we have developed a method to increase the binding capacity and efficiency of hybridization of DNA on to

derivatized glass surfaces. This makes use of the synergistic effect of two binding interactions between the **nucleic acids** and the coating chemicals on the surface of the glass slides. The enhanced binding allows the **nucleic acids** to be bound tightly and to survive stringency washes. When immobilized, DNA exhibits a higher propensity for hybridization on the surface than on slides with only one binding chemical. By varying the silane concentrations, we have shown that maximal DNA oligonucleotide binding on glass surfaces occurs when the percentage composition of both of the surface-coating chemicals falls to 0.2%, which is different from that on binding PCR products. This new mixture-combination approach for **nucleic-acid** binding allows signals from immobilization and hybridization to have higher signal-to-**noise** ratios than for other silane-coated methods.

L4 ANSWER 4 OF 29 MEDLINE on STN DUPLICATE 1
Full Text
AN 2003268584 IN-PROCESS
DN PubMed ID: 12706560
TI High-density, microsphere-based fiber optic DNA **microarrays**.
AU Epstein Jason R; Leung Amy P K; Lee Kyong Hoon; Walt David R
CS The Max Tishler Laboratory for Organic Chemistry, Tufts University, Medford, MA 02155, USA.
SO Biosensors & bioelectronics, (2003 May) 18 (5-6) 541-6.
Journal code: 9001289. ISSN: 0956-5663.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20030611
Last Updated on STN: 20031218
AB A high-density fiber optic DNA **microarray** has been developed consisting of oligonucleotide-functionalized, 3.1-microm-diameter microspheres randomly distributed on the etched face of an imaging fiber bundle. The fiber bundles are comprised of 6000-50000 fused optical fibers and each fiber terminates with an etched well. The microwell **array** is capable of housing complementary-sized microspheres, each containing thousands of copies of a unique oligonucleotide **probe** sequence. The **array** fabrication process results in random microsphere placement. Determining the position of microspheres in the random **array** requires an optical encoding scheme. This **array** platform provides many advantages over other **array** formats. The microsphere-stock suspension concentration added to the etched fiber can be controlled to provide inherent sensor redundancy. Examining identical microspheres has a beneficial effect on the signal-to-**noise** ratio. As other sequences of interest are discovered, new microsphere sensing elements can be added to existing microsphere pools and new **arrays** can be fabricated incorporating the new sequences without altering the existing detection capabilities. These **microarrays** contain the smallest feature sizes (3 microm) of any DNA **array**, allowing interrogation of extremely small sample volumes. Reducing the feature size results in higher local target molecule concentrations, creating rapid and highly sensitive assays. The microsphere **array** platform is also flexible in its applications; research has included DNA-protein interaction profiles, microbial strain differentiation, and non-labeled target interrogation with molecular beacons. Fiber optic microsphere-based DNA **microarrays** have a simple fabrication protocol enabling their expansion into other applications, such as single cell-based assays.

L4 ANSWER 5 OF 29 MEDLINE on STN DUPLICATE 2
Full Text

AN 2003398186 MEDLINE
DN 22816857 PubMed ID: 12938086
TI Genotyping African haplotypes in ATM using a co-spotted single-base extension assay.
AU Jain Maneesh; Thorstenson Yvonne R; Faulkner David M; Pourmand Nader; Jones Ted; Au Melinda; Oefner Peter J; White Kevin P; Davis Ronald W
CS Stanford Genome Technology Center, Palo Alto, California 94304, USA.
NC HG00205 (NHGRI)
SO HUMAN MUTATION, (2003 Sep) 22 (3) 214-21.
Journal code: 9215429. ISSN: 1098-1004.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200310
ED Entered STN: 20030826
Last Updated on STN: 20031028
Entered Medline: 20031027
AB Human genetic analysis, including population genetic studies, increasingly calls for cost-effective, high-throughput methods for the rapid screening of single nucleotide polymorphisms (SNPs) across many individuals. The modified single-base extension assay described here (arrayed SBE) is a highly accurate and robust method for SNP genotyping that can deliver genotypes at 3.5 cents each, following PCR. Specifically, amino-modified **probe**/target pairs were prehybridized, then co-spotted in a **microarray** format prior to enzymatic addition of allele-specific nucleotides. **Probe**/target identity was determined solely by its physical location on the **array** rather than by hybridization to a complementary target, resulting in a call rate of 99-100%. These innovations result in an inexpensive, accurate assay with exceptional signal-to-**noise** ratios, depending on the glass surface employed. Comparison of glass slides from three different manufacturers indicated that aldehyde-based Zyomyx slides provided superior performance for this assay. Arrayed SBE was applied to study the geographic distribution of three African-specific haplotypes in the human ATM gene. Four selectively neutral markers, which define the haplotypes H5, H6, and H7, were screened in a total of 415 individuals. Region-specific haplotype frequencies were consistent with patterns of human migration across and outside of Africa, suggesting a possible haplotype origin in East Africa. Arrayed SBE was a robust tool for this analysis that could be applied to any situation requiring the genotyping of a few SNPs in many individuals.

L4 ANSWER 6 OF 29 MEDLINE on STN
Full Text
AN 2003386278 MEDLINE
DN 22804540 PubMed ID: 12799473
TI Quantitative assessment of the importance of dye switching and biological replication in cDNA **microarray** studies.
AU Liang Mingyu; Briggs Amy G; Rute Elizabeth; Greene Andrew S; Cowley Allen W Jr
CS Department of Physiology, Medical College of Wisconsin, Milwaukee, Wisconsin 53226, USA.. mliang@mcw.edu
NC HL-29587 (NHLBI)
HL-54998 (NHLBI)
HL-66579 (NHLBI)
SO Physiol Genomics, (2003 Aug 15) 14 (3) 199-207.
Journal code: 9815683. ISSN: 1531-2267.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)

(VALIDATION STUDIES)
LA English
FS Priority Journals
EM 200310
ED Entered STN: 20030819
Last Updated on STN: 20031004
Entered Medline: 20031003

AB Dye switching and biological replication substantially increase the cost and the complexity of cDNA **microarray** studies. The objective of the present analysis was to quantitatively assess the importance of these procedures to provide a quantitative basis for decision-making in the design of **microarray** experiments. Taking advantage of the unique characteristics of a published data set, the impact of these procedures on the reliability of **microarray** results was calculated. Adding a second **microarray** with dye switching substantially increased the correlation coefficient between observed and predicted ln(ratio) values from 0.38 +/- 0.06 to 0.62 +/- 0.04 (n = 12) and the **outlier** concordance from 21 +/- 3% to 43 +/- 4%. It also increased the correlation with the entire set of **microarrays** from 0.60 +/- 0.04 to 0.79 +/- 0.04 and the **outlier** concordance from 31 +/- 6% to 58 +/- 5% and tended to improve the correlation with Northern blot results. Adding a second **microarray** to include biological replication also improved the performance of these indices but often to a lesser degree. Inclusion of both procedures in the second **microarray** substantially improved the consistency with the entire set of **microarrays** but had minimal effect on the consistency with predicted results. Analysis of another data set generated using a different cDNA labeling method also supported a significant impact of dye switching. In conclusion, both dye switching and biological replication substantially increased the reliability of **microarray** results, with dye switching likely having even greater benefits. Recommendations regarding the use of these procedures were proposed.

L4 ANSWER 7 OF 29 MEDLINE on STN
Full Text
AN 2003317445 MEDLINE
DN 22730773 PubMed ID: 12803655
TI The construction and use of bacterial DNA **microarrays** based on an optimized two-stage PCR strategy.
AU Postier Bradley L; Wang Hong-Liang; Singh Abhay; Impson Lori; Andrews Heather L; Klahn Jessica; Li Hong; Risinger George; Pesta David; Deyholos Michael; Galbraith David W; Sherman Louis A; Burnap Robert L
CS Department of Microbiology & Molecular Genetics, Oklahoma State University, Stillwater, OK 74078 USA.. postier@biochem.okstate.edu
SO BMC Genomics, (2003 Jun 12) 4 (1) 23.
Journal code: 100965258. ISSN: 1471-2164.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200307
ED Entered STN: 20030709
Last Updated on STN: 20030729
Entered Medline: 20030728

AB BACKGROUND: DNA **microarrays** are a powerful tool with important applications such as global gene expression profiling. Construction of bacterial DNA **microarrays** from genomic sequence data using a two-stage PCR amplification approach for the production of arrayed DNA is attractive because it allows, in principal, the continued re-amplification of DNA fragments and facilitates further utilization of the DNA fragments for additional uses (e.g. over-expression of protein). We describe the

successful construction and use of DNA **microarrays** by the two-stage amplification approach and discuss the technical challenges that were met and resolved during the project. RESULTS: Chimeric primers that contained both gene-specific and shared, universal sequence allowed the two-stage amplification of the 3,168 genes identified on the genome of Synechocystis sp. PCC6803, an important prokaryotic model organism for the study of oxygenic photosynthesis. The gene-specific component of the primer was of variable length to maintain uniform annealing temperatures during the 1st round of PCR synthesis, and situated to preserve full-length ORFs. Genes were truncated at 2 kb for efficient amplification, so that about 92% of the PCR fragments were full-length genes. The two-stage amplification had the additional advantage of normalizing the yield of PCR products and this improved the uniformity of DNA features robotically deposited onto the **microarray** surface. We also describe the techniques utilized to optimize hybridization conditions and signal-to-**noise** ratio of the transcription profile. The inter-lab transportability was demonstrated by the virtual error-free amplification of the entire genome complement of 3,168 genes using the universal primers in partner labs. The printed slides have been successfully used to identify differentially expressed genes in response to a number of environmental conditions, including salt stress. CONCLUSIONS: The technique detailed here minimizes the cost and effort to replicate a PCR-generated DNA gene fragment library and facilitates several downstream processes (e.g. directional cloning of fragments and gene expression as affinity-tagged fusion proteins) beyond the primary objective of producing DNA **microarrays** for global gene expression profiling.

L4 ANSWER 8 OF 29 MEDLINE on STN

Full Text

AN 2003072119 MEDLINE

DN 22470257 PubMed ID: 12582259

TI Three color cDNA **microarrays**: quantitative assessment through the use of fluorescein-labeled **probes**.

AU Hessner Martin J; Wang Xujing; Hulse Katie; Meyer Lisa; Wu Yan; Nye Steven; Guo Sun-Wei; Ghosh Soumitra

CS The Max McGee National Research Center for Juvenile Diabetes, The Medical College of Wisconsin and Children's Hospital of Wisconsin, 8701 Watertown Plank Road, Milwaukee, WI 53226, USA.. mhessner@mcw.edu

SO NUCLEIC ACIDS RESEARCH, (2003 Feb 15) 31 (4) e14.
Journal code: 0411011. ISSN: 1362-4962.

CY England: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 200303

ED Entered STN: 20030214
Last Updated on STN: 20030304
Entered Medline: 20030303

AB Gene expression studies using **microarrays** have great potential to generate new insights into human disease pathogenesis, but data quality remains a major obstacle. In particular, there does not exist a method to determine prior to hybridization whether an **array** will yield high quality data, given good study design and target preparation. We have solved this problem through development of a three-color cDNA **microarray** platform where printed **probes** are fluorescein labeled, but are spectrally compatible with Cy3 and Cy5 dye-labeled targets when using confocal laser scanners possessing narrow bandwidths. This approach enables prehybridization evaluation of **array**/spot morphology, DNA deposition and retention and background levels. By using these measurements and the intra-slide coefficient of variation for fluorescence

intensity we show that slides in the same batch are not equivalent and measurable prehybridization parameters can be predictive of hybridization performance as determined by replicate consistency. When hybridizing target derived from two cell lines to high and low quality replicate pairs (n = 50 pairs), a direct and significant relationship between prehybridization signal-to-background **noise** and post-hybridization reproducibility (R2 = 0.80, P < 0.001) was observed. We therefore conclude that slide selection based upon prehybridization quality scores will greatly benefit the ability to generate reliable gene expression data.

L4 ANSWER 9 OF 29 MEDLINE on STN
Full Text
AN 2003318590 MEDLINE
DN 22730761 PubMed ID: 12659661
TI Effects of mRNA amplification on gene expression ratios in cDNA experiments estimated by analysis of variance.
AU Nygaard Vigdis; Loland Anders; Holden Marit; Langaas Mette; Rue Havard; Liu Fang; Myklebost Ola; Fodstad Oystein; Hovig Eivind; Smith-Sorensen Birgitte
CS Department of Tumor Biology, Institute for Cancer Research, The Norwegian Radium Hospital, Montebello, 0310 Oslo, Norway.. vigdisny@radium.uio.no
SO BMC Genomics, (2003 Mar 23) 4 (1) 11.
Journal code: 100965258. ISSN: 1471-2164.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200307
ED Entered STN: 20030710
Last Updated on STN: 20030726
Entered Medline: 20030725
AB BACKGROUND: A limiting factor of cDNA **microarray** technology is the need for a substantial amount of RNA per labeling reaction. Thus, 20-200 micro-grams total RNA or 0.5-2 micro-grams poly (A) RNA is typically required for monitoring gene expression. In addition, gene expression profiles from large, heterogeneous cell populations provide complex patterns from which biological data for the target cells may be difficult to extract. In this study, we chose to investigate a widely used mRNA amplification protocol that allows gene expression studies to be performed on samples with limited starting material. We present a quantitative study of the variation and **noise** present in our data set obtained from experiments with either amplified or non-amplified material. RESULTS: Using analysis of variance (ANOVA) and multiple hypothesis testing, we estimated the impact of amplification on the preservation of gene expression ratios. Both methods showed that the gene expression ratios were not completely preserved between amplified and non-amplified material. We also compared the expression ratios between the two cell lines for the amplified material with expression ratios between the two cell lines for the non-amplified material for each gene. With the aid of multiple t-testing with a false discovery rate of 5%, we found that 10% of the genes investigated showed significantly different expression ratios. CONCLUSION: Although the ratios were not fully preserved, amplification may prove to be extremely useful with respect to characterizing low expressing genes.

L4 ANSWER 10 OF 29 MEDLINE on STN
Full Text
AN 2002313575 MEDLINE
DN 22001660 PubMed ID: 12005798

TI DNA hybridization to mismatched templates: a chip study.
AU Naef Felix; Lim Daniel A; Patil Nila; Magnasco Marcelo
CS Center for Studies in Physics and Biology, Rockefeller University, 1230 York Avenue, New York, New York 10021, USA.
SO Phys Rev E Stat Nonlin Soft Matter Phys, (2002 Apr) 65 (4 Pt 1) 040902. Journal code: 101136452. ISSN: 1539-3755.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200211
ED Entered STN: 20020612
Last Updated on STN: 20030105
Entered Medline: 20021108
AB High-density oligonucleotide **arrays** are among the most rapidly expanding technologies in biology today. In the GeneChip system, the reconstruction of the sample mRNA concentrations depends upon the differential signal generated by hybridizing the RNA to two nearly identical templates: a perfect match **probe** (PM) containing the exact biological sequence; and a single mismatch (MM) differing from the PM by a single base substitution. It has been observed that a large fraction of MMs repetitively bind targets better than the PMs, against the obvious expectation of sequence specificity. We examine this problem via statistical analysis of a large set of **microarray** experiments. We classify the **probes** according to their signal to **noise** (S/N) ratio, defined as the eccentricity of a (PM,MM) pair's "trajectory" across many experiments. Of those **probes** having large S/N (>3) only a fraction behave consistently with the commonly assumed hybridization model. Our results imply that the physics of DNA hybridization in **microarrays** is more complex than expected, and suggest estimators for the target RNA concentration.

L4 ANSWER 11 OF 29 MEDLINE on STN
Full Text
AN 2002647896 MEDLINE
DN 22295011 PubMed ID: 12388780
TI Quantitative **noise** analysis for gene expression **microarray** experiments.
AU Tu Y; Stolovitzky G; Klein U
CS IBM T. J. Watson Research Center, Yorktown Heights, NY 10598, USA..
yuhai@us.ibm.com
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2002 Oct 29) 99 (22) 14031-6. Journal code: 7505876. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200212
ED Entered STN: 20021031
Last Updated on STN: 20030105
Entered Medline: 20021209
AB A major challenge in DNA **microarray** analysis is to effectively dissociate actual gene expression values from experimental **noise**. We report here a detailed **noise** analysis for oligonuleotide-based **microarray** experiments involving reverse transcription, generation of labeled cRNA (target) through in vitro transcription, and hybridization of the target to the **probe** immobilized on the substrate. By designing sets of replicate experiments that bifurcate at different steps of the assay, we are able to separate the **noise** caused by sample preparation and the hybridization processes. We quantitatively characterize the strength of these different sources of **noise** and their respective dependence on the

gene expression level. We find that the sample preparation **noise** is small, implying that the amplification process during the sample preparation is relatively accurate. The hybridization **noise** is found to have very strong dependence on the expression level, with different characteristics for the low and high expression values. The hybridization **noise** characteristics at the high expression regime are mostly Poisson-like, whereas its characteristics for the small expression levels are more complex, probably due to cross-hybridization. A method to evaluate the significance of gene expression fold changes based on **noise** characteristics is proposed.

L4 ANSWER 12 OF 29 MEDLINE on STN DUPLICATE 3
Full Text
AN 2002613680 MEDLINE
DN 22258032 PubMed ID: 12370806
TI Mathematical modeling of **noise** and discovery of genetic expression classes in gliomas.
AU Fathallah-Shaykh Hassan M; Rigen Mo; Zhao Li-Juan; Bansal Kanti; He Bin; Engelhard Herbert H; Cerullo Leonard; Roenn Kelvin Von; Byrne Richard; Munoz Lorenzo; Rosseau Gail L; Glick Roberta; Lichtor Terry; DiSavino Elia
CS Department of Neurological Sciences, Rush Presbyterian-St. Lukes Medical Center, Chicago, Illinois, IL 60612, USA.. hfathall@rush.edu
NC R01-CA81367 (NCI)
R29-CA78825 (NCI)
SO ONCOGENE, (2002 Oct 17) 21 (47) 7164-74.
Journal code: 8711562. ISSN: 0950-9232.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200211
ED Entered STN: 20021010
Last Updated on STN: 20021213
Entered Medline: 20021104
AB The **microarray array** experimental system generates noisy data that require validation by other experimental methods for measuring gene expression. Here we present an algebraic modeling of **noise** that extracts expression measurements true to a high degree of confidence. This work profiles the expression of 19 200 cDNAs in 35 human gliomas; the experiments are designed to generate four replicate spots/gene with switching of **probes**. The validity of the extracted measurements is confirmed by: (1) cluster analysis that generates a molecular classification differentiating glioblastoma from lower-grade tumors and radiation necrosis; (2) By what other investigators have reported in gliomas using paradigms for assaying molecular expression other than gene profiling; and (3) Real-time RT-PCR. The results yield a genetic analysis of gliomas and identify classes of genetic expression that link novel genes to the biology of gliomas.

L4 ANSWER 13 OF 29 MEDLINE on STN
Full Text
AN 2002246634 MEDLINE
DN 21975967 PubMed ID: 11985315
TI High-density fiber-optic genosensor microsphere **array** capable of zeptomole detection limits.
AU Epstein Jason R; Lee Myoyong; Walt David R
CS The Max Tishler Laboratory for Organic Chemistry, Department of Chemistry, Tufts University, Medford, Massachusetts 02155, USA.
NC GM48142 (NIGMS)
SO ANALYTICAL CHEMISTRY, (2002 Apr 15) 74 (8) 1836-40.

Journal code: 0370536. ISSN: 0003-2700.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200205
ED Entered STN: 20020503
Last Updated on STN: 20020528
Entered Medline: 20020523

AB The detection limit of a fiber-optic microsensor **array** was investigated for simultaneous detection of multiple DNA sequences. A random **array** composed of oligonucleotide-functionalized 3.1-microm-diameter microspheres on the distal face of a 500-microm etched imaging fiber was monitored for binding to fluorescently labeled complementary DNA sequences. Inherent sensor redundancy in the **microarray** allows the use of multiple microspheres to increase the signal-to-**noise** ratio, further enhancing the detection capabilities. Specific hybridization was observed for each of three sequences in an **array** yielding a detection limit of 10(-21) mol (approximately 600 DNA molecules).

L4 ANSWER 14 OF 29 MEDLINE on STN DUPLICATE 4
Full Text

AN 2002727931 MEDLINE
DN 22378296 PubMed ID: 12490448
TI Statistical analysis of high-density oligonucleotide **arrays**: a multiplicative **noise** model.

AU Sasik R; Calvo E; Corbeil J
CS School of Medicine, University of California San Diego, La Jolla, CA 92093-0679, USA.. sasik@corgon.ucsd.edu

NC AI36214 (NIAID)
AI46237 (NIAID)
AI47703 (NIAID)
SO BIOINFORMATICS, (2002 Dec) 18 (12) 1633-40.
Journal code: 9808944. ISSN: 1367-4803.
CY England: United Kingdom
DT (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
(VALIDATION STUDIES)
LA English
FS Priority Journals
EM 200307
ED Entered STN: 20021220
Last Updated on STN: 20030703
Entered Medline: 20030702

AB MOTIVATION: High-density oligonucleotide **arrays** (GeneChip, Affymetrix, Santa Clara, CA) have become a standard research tool in many areas of biomedical research. They quantitatively monitor the expression of thousands of genes simultaneously by measuring fluorescence from gene-specific targets or **probes**. The relationship between signal intensities and transcript abundance as well as normalization issues have been the focus of much recent attention (Hill et al., 2001; Chudin et al., 2002; Naef et al., 2002a). It is desirable that a researcher has the best possible analytical tools to make the most of the information that this powerful technology has to offer. At present there are three analytical methods available: the newly released Affymetrix **Microarray** Suite 5.0 (AMS) software that accompanies the GeneChip product, the method of Li and Wong (LW; Li and Wong, 2001), and the method of Naef et al. (FN; Naef et al., 2001). The AMS method is tailored for analysis of a single **microarray**, and can therefore be used with any experimental design. The LW method on the other hand depends on a large number of **microarrays** in

an experiment and cannot be used for an isolated **microarray**, and the FN method is particular to paired **microarrays**, such as resulting from an experiment in which each 'treatment' sample has a corresponding 'control' sample. Our focus is on analysis of experiments in which there is a series of samples. In this case only the AMS, LW, and the method described in this paper can be used. The present method is model-based, like the LW method, but assumes multiplicative not additive **noise**, and employs elimination of statistically significant **outliers** for improved results. Unlike LW and AMS, we do not assume **probe**-specific background (measured by the so-called mismatch **probes**). Rather, we assume uniform background, whose level is estimated using both the mismatch and perfect match **probe** intensities. RESULTS: We present a new method for GeneChip analysis, based on a statistical model with multiplicative **noise**. We demonstrated that this method yields results superior to those obtained by the Affymetrix **Microarray** Suite 5.0 software and to those obtained by the model-based method of Li and Wong (Li and Wong, 2001). The present method eliminates the hard-to-interpret negative expression indices, and the binary 'presence' calls (present or absent) are replaced by the statistical significance (p-value) of gene expression. We have found that thresholding the p-values at the (0.1)(16)-level produces about the same number of 'present' calls as the AMS software. By testing our method on a pair of replicate GeneChips (hybridized with the same cRNA), we found that 95.6% of data points lie within the 1.25-fold interval. In other words, our method had a 4.4% type I error rate at the 1.25-fold level. The error rate of the LW method was 15%, and that of the AMS method was 29%. There were no points outside the 2-fold interval with the present method. Analysis of variance (ANOVA) of another experiment with multiple replicates shows that this reduction of variance is not accompanied by a corresponding reduction of signal. On the contrary, the signal-to-**noise** ratio (as measured by the distribution of F-statistics) of the present method is on average 3.4-times better than that of AMS, and 1.4-times better than that of Li and Wong.

L4 ANSWER 15 OF 29 MEDLINE on STN DUPLICATE 5
Full Text
AN 2002727927 MEDLINE
DN 22378291 PubMed ID: 12490443
TI Analysis of high density expression **microarrays** with signed-rank call algorithms.
AU Liu W-m; Mei R; Di X; Ryder T B; Hubbell E; Dee S; Webster T A; Harrington C A; Ho M-h; Baid J; Smeekens S P
CS Applied Research and Product Development, Affymetrix, Inc, 3380 Central Expressway, Santa Clara, CA 95051, USA.. wei-min liu@affymetrix.com
SO BIOINFORMATICS, (2002 Dec) 18 (12) 1593-9.
Journal code: 9808944. ISSN: 1367-4803.
CY England: United Kingdom
DT (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
(VALIDATION STUDIES)
LA English
FS Priority Journals
EM 200307
ED Entered STN: 20021220
Last Updated on STN: 20030703
Entered Medline: 20030702
AB MOTIVATION: We consider the detection of expressed genes and the comparison of them in different experiments with the high-density oligonucleotide **microarrays**. The results are summarized as the detection calls and comparison calls, and they should be robust against data **outliers** over a wide target concentration range. It is also

helpful to provide parameters that can be adjusted by the user to balance specificity and sensitivity under various experimental conditions. RESULTS: We present rank-based algorithms for making detection and comparison calls on expression **microarrays**. The detection call algorithm utilizes the discrimination scores. The comparison call algorithm utilizes intensity differences. Both algorithms are based on Wilcoxon's signed-rank test. Several parameters in the algorithms can be adjusted by the user to alter levels of specificity and sensitivity. The algorithms were developed and analyzed using spiked-in genes arrayed in a Latin square format. In the call process, p-values are calculated to give a confidence level for the pertinent hypotheses. For comparison calls made between two **arrays**, two primary normalization factors are defined. To overcome the difficulty that constant normalization factors do not fit all **probe** sets, we perturb these primary normalization factors and make increasing or decreasing calls only if all resulting p-values fall within a defined critical region. Our algorithms also automatically handle scanner saturation.

L4 ANSWER 16 OF 29 MEDLINE on STN
Full Text
AN 2002431550 MEDLINE
DN 22175205 PubMed ID: 12187936
TI Application of cDNA **microarray** technology to in vitro toxicology and the selection of genes for a real-time RT-PCR-based screen for oxidative stress in Hep-G2 cells.
AU Morgan Kevin T; Ni Hong; Brown H Roger; Yoon Lawrence; Qualls Charles W Jr; Crosby Lynn M; Reynolds Randall; Gaskill Betty; Anderson Steven P; Kepler Thomas B; Brainard Tracy; Liv Nik; Easton Marilyn; Merrill Christine; Creech Don; Sprenger Dirk; Conner Gary; Johnson Paul R; Fox Tony; Sartor Maureen; Richard Erika; Kuruvilla Sabu; Casey Warren; Benavides Gina
CS Aventis Pharmaceuticals, Raleigh, North Carolina 27604, USA..
kevin.morgan@aventis.com
SO TOXICOLOGIC PATHOLOGY, (2002 Jul-Aug) 30 (4) 435-51.
Journal code: 7905907. ISSN: 0192-6233.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200303
ED Entered STN: 20020822
Last Updated on STN: 20030313
Entered Medline: 20030312
AB Large-scale analysis of gene expression using cDNA **microarrays** promises the rapid detection of the mode of toxicity for drugs and other chemicals. cDNA **microarrays** were used to examine chemically induced alterations of gene expression in HepG2 cells exposed to a diverse group of toxicants at an equitoxic exposure concentration. The treatments were ouabain (43 microM), lauryl sulfate (260 microM), dimethylsulfoxide (1.28 M), cycloheximide (62.5 microM), tolbutamide (12.8 mM), sodium fluoride (3 mM), diethyl maleate (1.25 mM), buthionine sulfoximine (30 mM), potassium bromate (2.5 mM), sodium selenite (30 microM), alloxan (130 mM), adriamycin (40 microM), hydrogen peroxide (4 mM), and heat stress (45 degrees C x 30 minutes). Patterns of gene expression were correlated with morphologic and biochemical indicators of toxicity. Gene expression responses were characteristically different for each treatment. Patterns of expression were consistent with cell cycle arrest, DNA damage, diminished protein synthesis, and oxidative stress. Based upon these results, we concluded that gene expression changes provide a useful indicator of oxidative stress, as assessed by the GSH:GSSG ratio. Under

the conditions of this cell culture test system, oxidative stress upregulated 5 genes, HMOX1, p21(waf1/cip1), GCLM, GR, TXNR1 while downregulating CYP1A1 and TOPO2A. Primers and **probes** for these genes were incorporated into the design of a 7-gene plate for RT-PCR. The plate design permitted statistical analysis and allowed clear discrimination between chemicals inducing oxidative vs nonoxidative stress. A simple oxidative stress score (0-1), based on the responses by the 7 genes (including p-value) on the RT-PCR plate, was correlated with the GSH:GSSG ratio using linear regression and ranking (Pearson product) procedures. These analyses yielded correlation coefficients of 0.74 and 0.87, respectively, for the treatments tested (when 1 **outlier** was excluded), indicating a good correlation between the biochemical and transcriptional measures of oxidative stress. We conclude that it is essential to measure the mechanism of interest directly in the test system being used when assessing gene expression as a tool for toxicology. Tables 1-15, referenced in this paper, are not printed in this issue of Toxicologic Pathology. They are available as downloadable text files at http://taylorandfrancis.metapress.com/openurl.asp?genre=journal&issn=0192-6233. To access them, click on the issue link for 30(4), then select this article. A download option appears at the bottom of this abstract. In order to access the full article online, you must either have an individual subscription or a member subscription accessed through www.toxpath.org.

L4 ANSWER 17 OF 29 MEDLINE on STN
Full Text
AN 2002342845 MEDLINE
DN 22081218 PubMed ID: 12085637
TI **Microarray** image spot segmentation using the method of projections.
AU Stanley R J; Gattapulli M; Caldwell C W
CS Department of Electrical and Computer Engineering, 127 Emerson Electric Co. Hall, University of Missouri-Rolla, Rolla, MO 65401, USA.
SO BIOMEDICAL SCIENCES INSTRUMENTATION, (2002) 38 387-92.
Journal code: 0140524. ISSN: 0067-8856.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200211
ED Entered STN: 20020628
Last Updated on STN: 20021211
Entered Medline: 20021106
AB **Microarray** technology is increasingly used as a means of high throughput analysis of human, non-human and plant genomes. Manual methods of **array** production using this technology lead to many inherent problems in the **microarray** image produced. The density of the spots in the images produced is very high, such that neighboring spots can overlap. The image background is often not uniform, containing **noise** that is often difficult to distinguish from actual spots. In this research, a projections-based approach is investigated for spot segmentation in paired radio **probe microarray** images. An important aspect of spot segmentation is the capability to perform corresponding spot-to-spot comparisons between the paired images. Experimental results are presented for spot segmentation in isolated and paired **microarray** images.

L4 ANSWER 18 OF 29 MEDLINE on STN
Full Text
AN 2002050400 MEDLINE
DN 21633821 PubMed ID: 11772632
TI Single-base-pair discrimination of terminal mismatches by using

oligonucleotide **microarrays** and neural network analyses.
AU Urakawa Hidetoshi; Noble Peter A; El Fantroussi Said; Kelly John J; Stahl David A
CS Department of Civil and Environmental Engineering, University of Washington, Seattle, Washington 98195, USA.
SO APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (2002 Jan) 68 (1) 235-44.
Journal code: 7605801. ISSN: 0099-2240.
(Investigators: Stahl D A, U WA, Seattle)
CY United States
DT (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Space Life Sciences
EM 200205
ED Entered STN: 20020125
Last Updated on STN: 20020515
Entered Medline: 20020514
AB The effects of single-base-pair near-terminal and terminal mismatches on the dissociation temperature (T(d)) and signal intensity of short DNA duplexes were determined by using oligonucleotide **microarrays** and neural network (NN) analyses. Two perfect-match **probes** and 29 **probes** having a single-base-pair mismatch at positions 1 to 5 from the 5' terminus of the **probe** were designed to target one of two short sequences representing 16S rRNA. Nonequilibrium dissociation rates (i.e., melting profiles) of all **probe**-target duplexes were determined simultaneously. Analysis of variance revealed that position of the mismatch, type of mismatch, and formamide concentration significantly affected the T(d) and signal intensity. Increasing the concentration of formamide in the washing buffer decreased the T(d) and signal intensity, and it decreased the variability of the signal. Although T(d)s of **probe**-target duplexes with mismatches in the first or second position were not significantly different from one another, duplexes with mismatches in the third to fifth positions had significantly lower T(d)s than those with mismatches in the first or second position. The trained NNs predicted the T(d) with high accuracies (R(2) = 0.93). However, the NNs predicted the signal intensity only moderately accurately (R(2) = 0.67), presumably due to increased **noise** in the signal intensity at low formamide concentrations. Sensitivity analysis revealed that the concentration of formamide explained most (75%) of the variability in T(d)s, followed by position of the mismatch (19%) and type of mismatch (6%). The results suggest that position of the mismatch at or near the 5' terminus plays a greater role in determining the T(d) and signal intensity of duplexes than the type of mismatch.

L4 ANSWER 19 OF 29 MEDLINE on STN
Full Text
AN 2003506049 MEDLINE
DN PubMed ID: 12150713
TI Quantitative assessment of the use of modified nucleoside triphosphates in expression profiling: differential effects on signal intensities and impacts on expression ratios.
AU Nguyen Allen; Zhao Connie; Dorris David; Mazumder Abhijit
CS Motorola Life Sciences, 4088 Commercial Avenue, Northbrook, Illinois 60062, USA.. allenn1999@yahoo.com
SO BMC biotechnology [electronic resource], (2002 Jul 31) 2 (1) 14.
Journal code: 101088663. ISSN: 1472-6750.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals

EM 200312
ED Entered STN: 20031030
Last Updated on STN: 20031219
Entered Medline: 20031203
AB BACKGROUND: The power of DNA **microarrays** derives from their ability to monitor the expression levels of many genes in parallel. One of the limitations of such powerful analytical tools is the inability to detect certain transcripts in the target sample because of artifacts caused by background **noise** or poor hybridization kinetics. The use of base-modified analogs of nucleoside triphosphates has been shown to increase complementary duplex stability in other applications, and here we attempted to enhance **microarray** hybridization signal across a wide range of sequences and expression levels by incorporating these nucleotides into labeled cRNA targets. RESULTS: RNA samples containing 2-aminoadenosine showed increases in signal intensity for a majority of the sequences. These results were similar, and additive, to those seen with an increase in the hybridization time. In contrast, 5-methyluridine and 5-methylcytidine decreased signal intensities. Hybridization specificity, as assessed by mismatch controls, was dependent on both target sequence and extent of substitution with the modified nucleotide. Concurrent incorporation of modified and unmodified ATP in a 1:1 ratio resulted in significantly greater numbers of above-threshold ratio calls across tissues, while preserving ratio integrity and reproducibility. CONCLUSIONS: Incorporation of 2-aminoadenosine triphosphate into cRNA targets is a promising method for increasing signal detection in **microarrays**. Furthermore, this approach can be optimized to minimize impact on yield of amplified material and to increase the number of expression changes that can be detected.

L4 ANSWER 20 OF 29 MEDLINE on STN
Full Text
AN 2003505961 MEDLINE
DN PubMed ID: 11936955
TI Sources of variability and effect of experimental approach on expression profiling data interpretation.
AU Bakay Marina; Chen Yi-Wen; Borup Rehannah; Zhao Po; Nagaraju Kanneboyina; Hoffman Eric P
CS Research Center for Genetic Medicine, Children's National Medical Center, 111 Michigan Avenue, NW Washington, DC 20010 USA.. mbakay@cnmc.org
NC 5R01 NS29525-10 (NINDS)
UO1 HL66614-01 (NHLBI)
SO BMC bioinformatics [electronic resource], (2002) 3 (1) 4.
Journal code: 100965194. ISSN: 1471-2105.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200311
ED Entered STN: 20031030
Last Updated on STN: 20031219
Entered Medline: 20031118
AB BACKGROUND: We provide a systematic study of the sources of variability in expression profiling data using 56 RNAs isolated from human muscle biopsies (34 Affymetrix MuscleChip **arrays**), and 36 murine cell culture and tissue RNAs (42 Affymetrix U74Av2 **arrays**). RESULTS: We studied muscle biopsies from 28 human subjects as well as murine myogenic cell cultures, muscle, and spleens. Human MuscleChip **arrays** (4,601 **probe** sets) and murine U74Av2 Affymetrix **microarrays** were used for expression profiling. RNAs were profiled both singly, and as mixed groups. Variables studied included tissue heterogeneity, cRNA **probe** production,

patient diagnosis, and GeneChip hybridizations. We found that the greatest source of variability was often different regions of the same patient muscle biopsy, reflecting variation in cell type content even in a relatively homogeneous tissue such as muscle. Inter-patient variation was also very high (SNP **noise**). Experimental variation (RNA, cDNA, cRNA, or GeneChip) was minor. Pre-profile mixing of patient cRNA samples effectively normalized both intra- and inter-patient sources of variation, while retaining a high degree of specificity of the individual profiles (86% of statistically significant differences detected by absolute analysis; and 85% by a 4-pairwise comparison survival method). CONCLUSIONS: Using unsupervised cluster analysis and correlation coefficients of 92 RNA samples on 76 oligonucleotide **microarrays**, we found that experimental error was not a significant source of unwanted variability in expression profiling experiments. Major sources of variability were from use of small tissue biopsies, particularly in humans where there is substantial inter-patient variability (SNP **noise**).

L4 ANSWER 21 OF 29 MEDLINE on STN
Full Text
AN 2002080735 MEDLINE
DN 21665999 PubMed ID: 11806820
TI Characterization of the expression ratio **noise** structure in high-density oligonucleotide **arrays**.
AU Naef Felix; Hacker Coleen R; Patil Nila; Magnasco Marcelo
CS Mathematical Physics laboratory, Center for Studies in Physics and Biology, The Rockefeller University, 1230 York Ave, NY 10021, USA.. felix@funes.rockefeller.edu
SO GENOMEBIOLOGY.COM, (2002) 3 (1) PREPRINT0001.
Journal code: 100960660. ISSN: 1465-6914.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200205
ED Entered STN: 20020128
Last Updated on STN: 20030105
Entered Medline: 20020502
AB BACKGROUND: High-density oligonucleotide **microarrays** provide a powerful tool for assessing differential mRNA expression levels. Characterizing the **noise** resulting from the enzymatic and hybridization steps, called type I **noise**, is essential for attributing significance measures to the differential expression scores. We introduce scoring functions for expression ratios, and associated quality measures. Both the PM (Perfect Match) **probes** and PM-MM differentials (MM is the single MisMatch) are considered as raw intensities. We then characterize the log-ratio **noise** structure using robust estimates of their intensity dependent variance. RESULTS: We show the relationships between the obtained ratios and their quality measures. The complementarity of PM and PM-MM methods is emphasized by the **probe** sets signal to **noise** measures. Using a large set of replicate experiments, we demonstrate that the **noise** structure in the log-ratios very closely follows a local log-normal distribution for both the PM and PM-MM cases. Therefore, significance relative to the type I **noise** can be quantified reliably using the local STD. We discuss the intensity dependence of the STD and show that ratio scores >1.25 are significant in the mid- to high-intensity range. CONCLUSIONS: The ratio **noise** structure inherent to high-density oligonucleotide **arrays** can be well described in terms of local log-normal ratio distributions with characteristic intensity dependence. Therefore, robust estimates of the local STD of these distributions provide a simple and powerful way for assessing significance (relative to type I **noise**) in differential gene

expression. This approach will be helpful for improving the reliability of predictions from hybridization experiments in general.

L4 ANSWER 22 OF 29 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
Full Text
AN 2002:304319 BIOSIS
DN PREV200200304319
TI Sources of variability and effect of experimental approach on expression profiling data interpretation.
AU Bakay, Marina; Chen, Yi-Wen; Borup, Rehannah; Zhao, Po; Nagaraju, Kanneboyina; Hoffman, Eric P. [Reprint author]
CS Research Center for Genetic Medicine, Children's National Medical Center, 111 Michigan Avenue, N.W., Washington, DC, 20010, USA
mbakay@cnmc.org; ychen@cnmc.org; rborup@cnmc.org; pzhao@cnmcresearch.org; knagaraj@mail.jhmi.edu; ehoffman@cnmresearch.org
SO BMC Bioinformatics, (January 31, 2002) Vol. 3, No. 4 Cited April 17, 2002, pp. 1-12. http://www.biomedcentral.com/content/pdf/1471-2105-3-4.pdf. cited May 2, 2002. http://www.biomedcentral.com/1471-2105. online. ISSN: 1471-2105.
DT Article
LA English
ED Entered STN: 22 May 2002
Last Updated on STN: 22 May 2002
AB Background: We provide a systematic study of the sources of variability in expression profiling data using 56 RNAs isolated from human muscle biopsies (34 Affymetrix Muscle Chip **arrays**), and 36 murine cell culture and tissue RNAs (42 Affymetrix U74Av2 **arrays**). Results: We studied muscle biopsies from 28 human subjects as well as murine myogenic cell cultures, muscle, and spleens. Human MuscleChip **arrays** (4,601 **probe** sets) and murine U74Av2 Affymetrix **microarrays** were used for expression profiling. RNAs were profiled both singly, and as mixed groups. Variables studied included tissue heterogeneity, cRNA **probe** production, patient diagnosis, and GeneChip hybridizations. We found that the greatest source of variability was often different regions of the same patient muscle biopsy, reflecting variation in cell type content even in a relatively homogeneous tissue such as muscle. Inter-patient variation was also very high (SNP **noise**). Experimental variation (RNA, cDNA, cRNA, or GeneChip) was minor. Pre-profile mixing of patient cRNA samples effectively normalized both intra- and inter-patient sources of variation, while retaining a high degree of specificity of the individual profiles (86% of statistically significant differences detected by absolute analysis; and 85% by a 4-pairwise comparison survival method). Conclusions: Using unsupervised cluster analysis and correlation coefficients of 92 RNA samples on 76 oligonucleotide **microarrays**, we found that experimental error was not a significant source of unwanted variability in expression profiling experiments. Major sources of variability were from use of small tissue biopsies, particularly in humans where there is substantial inter-patient variability (SNP **noise**).

L4 ANSWER 23 OF 29 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
Full Text
AN 2003:325974 BIOSIS
DN PREV200300325974
TI GENETIC ANALYSIS OF HIGH - GRADE GLIOMAS.
AU Fathallah-Shaykh, H. M. [Reprint Author]; Rigen, M. [Reprint Author]; Zhao, L. J. [Reprint Author]; Bansal, K. [Reprint Author]; He, B. [Reprint Author]; Engelhard, H.; Cerullo, L.; Von Roenn, K.; Byrne, R.; Munoz, L.; Rosseau, G. L.; Glick, R.; Lichtor, T.; DiSavino, E. [Reprint Author]
CS Dept Neurolog Sci, Neurosurgery, Rush Med Ctr, Chicago, IL, USA
SO Society for Neuroscience Abstract Viewer and Itinerary Planner, (2002)

Vol. 2002, pp. Abstract No. 718.4. http://sfn.scholarone.com. cd-rom.
Meeting Info.: 32nd Annual Meeting of the Society for Neuroscience. Orlando, Florida, USA. November 02-07, 2002. Society for Neuroscience.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 16 Jul 2003
Last Updated on STN: 16 Jul 2003
AB The **microarray array** experimental system generates noisy data that require validation by other experimental methods for measuring gene expression. Here we present an algebraic modeling of **noise** that extracts expression measurements true to a high degree of confidence. This work profiles the expression of 19,200 cDNAs in 35 human gliomas; the experiments are designed to include 4 replicate spots/gene with switching of **probes**. The validity of the extracted measurements is confirmed by: 1) cluster analysis that generates a molecular classification differentiating glioblastoma from lower-grade tumors and radiation necrosis. 2) By what other investigators have reported in gliomas using paradigms for assaying molecular expression other than gene profiling. And 3) Real-time RT PCR. The results yield a genetic analysis of gliomas and identify classes of genetic expression that link novel genes to the biology of gliomas.

L4 ANSWER 24 OF 29 MEDLINE on STN DUPLICATE 6
Full Text
AN 2001406390 MEDLINE
DN 21351071 PubMed ID: 11457934
TI Monitoring signal transduction in cancer: cDNA **microarray** for semiquantitative analysis.
AU Hsieh H B; Lersch R A; Callahan D E; Hayward S; Wong M; Clark O H; Weier H U
CS Life Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, California, USA.
SO JOURNAL OF HISTOCHEMISTRY AND CYTOCHEMISTRY, (2001 Aug) 49 (8) 1057-8.
Journal code: 9815334. ISSN: 0022-1554.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200108
ED Entered STN: 20010806
Last Updated on STN: 20010806
Entered Medline: 20010802
AB This study targeted the development of a novel **microarray** tool to allow rapid determination of the expression levels of 58 different tyrosine kinase (tk) genes in small tumor samples. The goals were to define a reference **probe** for multi-sample comparison and to investigate the variability and reproducibility of the image acquisition and RT-PCR procedures. The small number of tk genes on our **arrays** enabled us to define a reference **probe** by artificially mixing all genes on the **arrays**. Such a **probe** provided contrast reference for comparative hybridization of control and sample DNA and enabled cross-comparison of more than two samples against one another. Comparison of signals generated from multiple scanning eliminated the concern of photo bleaching and scanner intrinsic **noise**. Tests performed with breast, thyroid, and prostate cancer samples yielded distinctive patterns and suggest the feasibility of our approach. Repeated experiments indicated reproducibility of such **arrays**. Up- or downregulated genes identified by this rapid screening are now being investigated with techniques such as in situ hybridization.

L4 ANSWER 25 OF 29 MEDLINE on STN
Full Text
AN 2001700078 MEDLINE
DN 21615120 PubMed ID: 11747614
TI Bayesian estimation of fold-changes in the analysis of gene expression: the PFOLD algorithm.
AU Theilhaber J; Bushnell S; Jackson A; Fuchs R
CS Aventis Pharmaceuticals, Cambridge Genomics Center, 26 Landsdowne Street, Cambridge, MA 02139, USA.. joachimtheilhaber@aventis.com
SO JOURNAL OF COMPUTATIONAL BIOLOGY, (2001) 8 (6) 585-614.
Journal code: 9433358. ISSN: 1066-5277.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200203
ED Entered STN: 20011219
Last Updated on STN: 20020305
Entered Medline: 20020304
AB A general and detailed **noise** model for the DNA **microarray** measurement of gene expression is presented and used to derive a Bayesian estimation scheme for expression ratios, implemented in a program called PFOLD, which provides not only an estimate of the fold-change in gene expression, but also confidence limits for the change and a P-value quantifying the significance of the change. Although the focus is on oligonucleotide **microarray** technologies, the scheme can also be applied to cDNA based technologies if parameters for the **noise** model are provided. The model unifies estimation for all signals in that it provides a seamless transition from very low to very high signal-to-**noise** ratios, an essential feature for current **microarray** technologies for which the median signal-to-**noise** ratios are always moderate. The dual use, as decision statistics in a two-dimensional space, of the P-value and the fold-change is shown to be effective in the ubiquitous problem of detecting changing genes against a background of unchanging genes, leading to markedly higher sensitivities, at equal selectivity, than detection and selection based on the fold-change alone, a current practice until now.

L4 ANSWER 26 OF 29 MEDLINE on STN
Full Text
AN 2001177068 MEDLINE
DN 21039019 PubMed ID: 11196312
TI Maximization of signal derived from cDNA **microarrays**.
AU Wildsmith S E; Archer G E; Winkley A J; Lane P W; Bugelski P J
CS SmithKline Beecham Pharmaceuticals, Hertfordshire, UK.. sophie e wildsmith@sbphrd.com
SO BIOTECHNIQUES, (2001 Jan) 30 (1) 202-6, 208.
Journal code: 8306785. ISSN: 0736-6205.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200103
ED Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010329
AB **Microarray** technology is a powerful tool for generating expression data on a large number of genes simultaneously. However, as for any assay, it must be reproducible to give confidence in the results. Using a classical statistical method--the factorial design of experiments--we have assessed

the effects of different experimental factors in our system. Significant effects on signal were seen when the standard components were substituted with a different enzyme, fluorescent label, or RNA purification method. This has led to the implementation of an improved procedure that maximizes signal without affecting the variability of the system, thus increasing the signal-to-**noise** ratio. In addition, we were able to quantify the variability between **microarrays** and replicates within **microarrays**.

L4 ANSWER 27 OF 29 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
Full Text
AN 2002:152018 BIOSIS
DN PREV200200152018
TI **Microarray** analysis of bone marrow cells from amifostine-treated AML patients and normal CD34+ bone marrow cells.
AU Galili, Naomi [Reprint author]; Dangerfield, Bruce [Reprint author]; John, Premila [Reprint author]; Semrad, Thomas [Reprint author]; Raza, Azra [Reprint author]; Preisler, Harvey [Reprint author]
CS Rush Cancer Institute, Rush-Presbyterian-St. Luke's Medical Center, Chicago, IL, USA
SO Blood, (November 16, 2001) Vol. 98, No. 11 Part 2, pp. 158b. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 2. Orlando, Florida, USA. December 07-11, 2001. American Society of Hematology.
CODEN: BLOOAW. ISSN: 0006-4971.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 21 Feb 2002
Last Updated on STN: 26 Feb 2002
AB Treatment failure of poor prognosis AML can be attributed to treatment resistance in a large proportion of the patients. We have shown that the administration of amifostine after the end of cytotoxic therapy can lead to an increase in CR or return to a pre-leukemia state in approximately 50% of the poor prognosis patients (accompanying abstract HD Preisler et al). In an attempt to further understand the molecular mechanisms by which amifostine reduces treatment resistance, we used **microarray** analysis to examine the gene expression changes in bone marrow mononuclear cells after patient treatment with amifostine. In addition, we compared the pre-treatment AML **microarray** profiles with those of CD34+ cells isolated from aspirates of normal donors. Chips containing 19K cDNAs obtained from the Ontario Cancer Institute were used for analysis. Total RNA (1-3ug) was amplified using a template-switch T7 protocol. Initial calibration using a reference **probe** composed of the pooled RNA of 11 cell lines was labeled with both Cy3 and Cy5 to establish the robustness of the system. Less than 5% **outliers** were found at a threshold of 1.5 fold change in expression ratio. This minimal variation may be due in part to the step-down hybridization temperatures (65degreeCfwdarw60degreeCfwdarw55degreeC) programmable with the Genomic Solution GeneTac hybridzation unit. The reproducibility of the amplification was established using a model system of total RNA from human heart and lung tissue. **Array** analysis of multiple independent amplifications of the heart and lung RNA (including reversals of Cy3 and Cy5 for **probe** preparation) resulted in very consistent gene expression profiles (average r=0.954) for the genes with expression ratio changes greater than 1.5. Amifostine (200mg/m2 IV) was administered to 7 patients with untreated AML and the gene expression patterns before and 3 days after amifostine treatment were generated. CD34+ cells, separated from 6 normal donor aspirates, were also analyzed. Expression ratios of the heart-lung model, the pooled cell lines, the CD34+ normal samples and the patient samples before and after amifostine treatment were all analyzed

using hierarchical clustering techniques. Preliminary analysis showed that there seemed to be substantial patient specific variation, as reported in other treatment studies. Detailed analysis of these patients and of the normal CD34+ cells will be reported.

L4 ANSWER 28 OF 29 MEDLINE on STN
Full Text
AN 2000464551 MEDLINE
DN 20469906 PubMed ID: 11013446
TI Oligonucleotide **microarray** based detection of repetitive sequence changes.
AU Hacia J G; Edgemon K; Fang N; Mayer R A; Sudano D; Hunt N; Collins F S
CS National Human Genome Research Institute, National Institutes of Health, Bethesda, Maryland 20892, USA.
SO HUMAN MUTATION, (2000 Oct) 16 (4) 354-63.
Journal code: 9215429. ISSN: 1098-1004.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200010
ED Entered STN: 20010322
Last Updated on STN: 20010521
Entered Medline: 20001027
AB Prior studies of oligonucleotide **microarray**-based mutational analysis have demonstrated excellent sensitivity and specificity except in circumstances where a frameshift mutation occurs in the context of a short repeated sequence. To further evaluate this circumstance, a series of **nucleic acid** samples having heterozygous mutations within repetitive BRCA1 sequence tracts was prepared and evaluated. These mutations included single nucleotide insertions and deletions in homopolymer runs, insertions and deletions of trinucleotide repeats, and duplications. Two-color comparative hybridization experiments were used wherein wild type reference and test targets are co-hybridized to **microarrays** designed to screen the entire BRCA1 coding sequence for all possible sequence changes. Mutations in simulated heterozygote samples were detected by observing relative losses of test target hybridization signal to select perfect match oligonucleotide **probes**. While heterozygous mutations could be readily distinguished above background **noise** in 9/19 cases, it was not possible to detect alterations in a poly dA/dT tract, small triplet repeat expansions, and a 10 bp direct repeat. Unexpectedly, samples containing (GAT)(3) triplet repeat expansions showed significantly higher affinity toward specific perfect match **probes** relative to their wild type counterparts. Therefore, markedly increased as well as decreased test sample hybridization to perfect match **probes** should be used to raise a suspicion of repetitive sequence changes.

L4 ANSWER 29 OF 29 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
Full Text
AN 2001:516854 BIOSIS
DN PREV200100516854
TI Estimation of the confidence limits of oligonucleotide **array**-based measurements of differential expression.
AU Wolber, Paul K. [Reprint author]; Atwell, Andrew S. [Reprint author]; Enderwick, Cynthia Y. [Reprint author]; Delenstarr, Glenda C. [Reprint author]; Dorsel, Andreas N. [Reprint author]; Shannon, Karen W. [Reprint author]; Kincaid, Robert H. [Reprint author]; Chen, Chao [Reprint author]; Schidel, Shad R. [Reprint author]; Aschoff, Michael P. [Reprint author]
CS Agilent Technologies, Palo Alto, CA, USA

SO International Genome Sequencing and Analysis Conference, (2000) Vol. 12, pp. 98. print.
Meeting Info.: 12th International Genome Sequencing and Analysis Conference. Miami Beach, Florida, USA. September 12-15, 2000.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 7 Nov 2001
Last Updated on STN: 23 Feb 2002
AB **Microarrays** of oligonucleotide **probes** can be used to simultaneously infer the differential expression states of many mRNA's in two samples. Such inferences are limited by systematic and random measurement errors. Systematic errors include signal gradients, imperfect feature morphologies, mismatched sample concentrations, cross-hybridization and scanner bias. Random errors arise from chemical and scanning **noise**, particularly for low signals. We have used a combination of two-color labeling (with fluor xchange) and rational **array** design to minimize systematic errors from gradients, imperfect features and mismatched sample concentrations. On-**array** specificity control **probes** and careful **probe** design were used to correct for cross-hybridization. Random errors were reduced via automated bad feature flagging and an advanced scanner design. We have scored feature significance, using established statistical tests. We have then estimated the intrinsic random measurement error as a function of average **probe** signal via sample self-comparison experiments (human K-562 cell mRNA). Finally, we have estimated the accuracy of differential expression measurements between K-562 cells and HeLa cells by evaluating the consistency with which different **probes** to the same mRNA measure differential expression. The data establish the importance of the use of sensitive **probes** and the elimination of systematic errors in producing reliable estimates of differential expression.

```
=> e delenstarr g/au
E1            2      DELENS NADIA/AU
E2            1      DELENSTAR GLENDA/AU
E3            0 --> DELENSTARR G/AU
E4            3      DELENSTARR GLENDA/AU
E5            3      DELENSTARR GLENDA C/AU
E6           16      DELENTDECKER P/AU
E7            4      DELENTDECKER PHILIPPE/AU
E8            1      DELENTDEKER P/AU
E9           14      DELENTE J/AU
E10           8      DELENTE J J/AU
E11           4      DELENTE JACQUES/AU
E12           2      DELENTE JACQUES J/AU

=> s e2-e5
L5            7 ("DELENSTAR GLENDA"/AU OR "DELENSTARR G"/AU OR "DELENSTARR GLEND
                A"/AU OR "DELENSTARR GLENDA C"/AU)

=> duplicate remove l5
PROCESSING COMPLETED FOR L5
L6            7 DUPLICATE REMOVE L5 (0 DUPLICATES REMOVED)

=> d 1-7 bib ab

L6   ANSWER 1 OF 7  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
Full Text
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AN 2002:489123 BIOSIS
DN PREV200200489123
TI Systems tools and methods of assaying biological materials using spatially-addressable arrays.
AU **Delenstarr, Glenda C.** [Inventor]
CS ASSIGNEE: Agilent Technologies, Inc.
PI US 6428957 August 06, 2002
SO Official Gazette of the United States Patent and Trademark Office Patents, (Aug. 6, 2002) Vol. 1261, No. 1. http://www.uspto.gov/web/menu/patdata.html. e-file.
CODEN: OGUPE7. ISSN: 0098-1133.
DT Patent
LA English
ED Entered STN: 18 Sep 2002
Last Updated on STN: 18 Sep 2002
AB Systems, tools and methods of assaying biological material are used to perform complex sandwich hybridization assays. The tools used comprise biological solution probes that are customized for each assay. The solution probe comprises a first region for hybridizing to a probe, in a generic set of capture probes on a universal assay apparatus, and a second region for hybridizing to a target in a sample. The solution probe assembles the target to the assay apparatus by hybridizing the second region to the target and the first region to the capture probe. In array assays, one or more biological samples, having one or more targets per sample, can be multiplexed on the same universal array comprising the generic set of capture probes in an array pattern of features on the substrate. The customized solution probe addresses and assembles a predetermined target-sample combination onto the array at a corresponding capture probe address location. The systems, tools and methods have specificity and sensitivity by systematically providing a reduced likelihood of cross-hybridizations and intramolecular structures in the probes. Specificity and sensitivity of the assay are provided by the incorporation of a chemically modified monomer in the capture probe and a similarly modified monomer complement in the first region of the solution probe. The modified monomers preferentially hybridize with each other. When the probe and respective probe region are oligonucleotides, the complementary modified nucleotides have a reversed polarity relative to the polarity of the respective probe and probe region. The complementary reversed polarity nucleotides form a thermodynamically more stable hybridization to each other than a hybridization between the reversed polarity nucleotide and a complementary nucleotide whose polarity is not similarly reversed.

L6 ANSWER 2 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
Full Text
AN 2001:402242 BIOSIS
DN PREV200100402242
TI Method for evaluating oligonucleotide probe sequences.
AU Shannon, Karen W. [Inventor]; Wolber, Paul K. [Inventor, Reprint author]; **Delenstarr, Glenda C.** [Inventor]; Webb, Peter G. [Inventor]; Kincaid, Robert H. [Inventor]
CS Los Altos, CA, USA
ASSIGNEE: Agilent Technologies, Inc.
PI US 6251588 June 26, 2001
SO Official Gazette of the United States Patent and Trademark Office Patents, (June 26, 2001) Vol. 1247, No. 4. e-file.
CODEN: OGUPE7. ISSN: 0098-1133.
DT Patent
LA English
ED Entered STN: 22 Aug 2001

Last Updated on STN: 22 Feb 2002

AB Methods are disclosed for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. A predetermined number of unique oligonucleotides is identified. The unique oligonucleotides are chosen to sample the entire length of a nucleotide sequence that is hybridizable with the target nucleotide sequence. At least one parameter that is independently predictive of the ability of each of the oligonucleotides of the set to hybridize to the target nucleotide sequence is determined and evaluated for each of the above oligonucleotides. A subset of oligonucleotides within the predetermined number of unique oligonucleotides is identified based on the evaluation of the parameter. Oligonucleotides in the subset are identified that are clustered along a region of the nucleotide sequence that is hybridizable to the target nucleotide sequence. The method may be carried out with the aid of a computer.

L6 ANSWER 3 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
Full Text

AN 2001:510448 BIOSIS

DN PREV200100510448

TI Analysis of steroid induced gene expression in multiple tissues using inkjet synthesized oligonucleotide microarrays.

AU Hwang, Stuart [Reprint author]; Rajkumar, Lakshmanaswamy; Xiao, Jenny; Guzman, Rafael; Brzoska, Pius; Yoshikawa, Matthew; Yang, Jason; **Delenstar, Glenda**; Chiou, Shiun-Kwei; Wolber, Paul K.; Shannon, Karen; Nandi, Satyabrata

CS Agilent, Palo Alto, CA, USA

SO Proceedings of the American Association for Cancer Research Annual Meeting, (March, 2001) Vol. 42, pp. 655. print.
Meeting Info.: 92nd Annual Meeting of the American Association for Cancer Research. New Orleans, LA, USA. March 24-28, 2001.
ISSN: 0197-016X.

DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)

LA English

ED Entered STN: 31 Oct 2001
Last Updated on STN: 23 Feb 2002

L6 ANSWER 4 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
Full Text

AN 2001:528512 BIOSIS

DN PREV200100528512

TI High-throughput microarray analysis: Automated multi-array scanning and feature extraction.

AU Cattell, Herb [Reprint author]; **Delenstarr, Glenda** [Reprint author]; Enderwick, Cynthia [Reprint author]; Kincaid, Robert [Reprint author]; Sampas, Nick [Reprint author]; Sillman, Debby [Reprint author]; Wolber, Paul [Reprint author]

CS Bioscience Products, Agilent Technologies, Palo Alto, CA, USA

SO International Genome Sequencing and Analysis Conference, (2000) Vol. 12, pp. 106. print.
Meeting Info.: 12th International Genome Sequencing and Analysis Conference. Miami Beach, Florida, USA. September 12-15, 2000.

DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)

LA English

ED Entered STN: 14 Nov 2001
Last Updated on STN: 23 Feb 2002

AB The analysis of microarrays has historically been an interactive task

requiring the user to manually scan and feature extract each array individually. Typical points of user interaction include defining the scan area, aligning a grid to enable the feature finding process, flagging anomalous features and/or regions within the array, and the management of various files including design or layout files, scan files, and results files. We designed an automated feature extraction system around our low detection limit, dual laser fluorescent scanner with autoloading capability. This approach allows the user to load a carousel with arrays and 'walkaway' from the system, which is left to scan and feature extract unattended in a pipelined fashion. The user returns later to find all arrays scanned, extracted and processed, and ready for further analysis. Through the use of fiducials and barcodes, which together define the scan area and locate the array in the scanned image, our system simplifies image processing and eliminates file management issues. Automated methods in the feature extractor replace the remaining interactive steps such as feature finding and flagging of outlier features. The processed results include normalized signals, gene expression ratios, and associated errors and p-values that can be used in downstream analysis.

L6 ANSWER 5 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
Full Text
AN 2001:516854 BIOSIS
DN PREV200100516854
TI Estimation of the confidence limits of oligonucleotide array-based measurements of differential expression.
AU Wolber, Paul K. [Reprint author]; Atwell, Andrew S. [Reprint author]; Enderwick, Cynthia Y. [Reprint author]; **Delenstarr, Glenda C.** [Reprint author]; Dorsel, Andreas N. [Reprint author]; Shannon, Karen W. [Reprint author]; Kincaid, Robert H. [Reprint author]; Chen, Chao [Reprint author]; Schidel, Shad R. [Reprint author]; Aschoff, Michael P. [Reprint author]
CS Agilent Technologies, Palo Alto, CA, USA
SO International Genome Sequencing and Analysis Conference, (2000) Vol. 12, pp. 98. print.
Meeting Info.: 12th International Genome Sequencing and Analysis Conference. Miami Beach, Florida, USA. September 12-15, 2000.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 7 Nov 2001
Last Updated on STN: 23 Feb 2002
AB Microarrays of oligonucleotide probes can be used to simultaneously infer the differential expression states of many mRNA's in two samples. Such inferences are limited by systematic and random measurement errors. Systematic errors include signal gradients, imperfect feature morphologies, mismatched sample concentrations, cross-hybridization and scanner bias. Random errors arise from chemical and scanning noise, particularly for low signals. We have used a combination of two-color labeling (with fluor xchange) and rational array design to minimize systematic errors from gradients, imperfect features and mismatched sample concentrations. On-array specificity control probes and careful probe design were used to correct for cross-hybridization. Random errors were reduced via automated bad feature flagging and an advanced scanner design. We have scored feature significance, using established statistical tests. We have then estimated the intrinsic random measurement error as a function of average probe signal via sample self-comparison experiments (human K-562 cell mRNA). Finally, we have estimated the accuracy of differential expression measurements between K-562 cells and HeLa cells by evaluating the consistency with which different probes to the same mRNA measure differential expression. The data establish the importance of the

use of sensitive probes and the elimination of systematic errors in producing reliable estimates of differential expression.

L6 ANSWER 6 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
Full Text
AN 2001:494497 BIOSIS
DN PREV200100494497
TI Performance characterization of cDNA microarrays produced by ink-jet deposition.
AU Amorese, Doug [Reprint author]; Bruhn, Laurakay [Reprint author]; Caren, Mike [Reprint author]; Collins, Scot [Reprint author]; DaQuino, Larry [Reprint author]; **Delenstarr, Glenda** [Reprint author]; Fisher, Bill [Reprint author]; Ilsley-Tyree, Diane [Reprint author]; Lightfoot, Samar [Reprint author]; Martins, Henrique [Reprint author]; Reyna, Stephanie [Reprint author]; Sampas, Nick [Reprint author]; Scheifer, Kyle [Reprint author]; Stanton, Larry [Reprint author]; Sum, Cristina [Reprint author]; Tella, Rich [Reprint author]; Templin, Cathy [Reprint author]; Villaneuva, Heidi [Reprint author]; Webb, Peter [Reprint author]; Wiest, Debra [Reprint author]; Westall, Mark [Reprint author]
CS Agilent Technologies, Palo Alto, CA, USA
SO International Genome Sequencing and Analysis Conference, (2000) Vol. 12, pp. 47. print.
Meeting Info.: 12th International Genome Sequencing and Analysis Conference. Miami Beach, Florida, USA. September 12-15, 2000.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 24 Oct 2001
Last Updated on STN: 23 Feb 2002
AB Microarray technology has developed as a versatile method to explore gene expression on a genome-wide scale. We have developed a process to print large volumes of high-density arrays of cDNAs onto modified glass surfaces by ink-jet deposition. Monitors on the deposition tool confirm delivery and placement of every probe solution onto the array. Our process has combined developments in nucleic acid deposition and image acquisition/analysis to produce high-quality cDNA arrays with a speed and economy possible only with a non-contact process. An understanding of system performance (array, scanner, software) is essential for meaningful interpretation of expression data derived from complex biological situations. To characterize the performance of our system, we have executed a series of controlled experiments designed to carefully measure reproducibility, sensitivity, and reliability of expression data. We have determined the variance of expression signals produced within and between arrays by comparing values generated from replicate samples in replicate experiments. The lowest limits of detection for transcripts in this system and accuracy of differential expression values were determined by analysis of titrated reference RNA samples. These results show that cDNA microarrays produced by our deposition process are capable of generating highly reliable expression data for thousands of genes simultaneously.

L6 ANSWER 7 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
Full Text
AN 2001:494487 BIOSIS
DN PREV200100494487
TI Transcriptional response of angiogenic endothelial cells assessed by cDNA microarrays.
AU Stanton, Larry [Reprint author]; Wolgemuth, Jay; Matcuk, George; Quertermous, Tom; Bruhn, Laurakay [Reprint author]; Amorese, Doug [Reprint author]; Caren, Mike [Reprint author]; Collins, Scot [Reprint author];

Delenstarr, Glenda [Reprint author]; Enderwick, Cynthia [Reprint author]; Reyna, Stephanie [Reprint author]; Ilsley, Diane [Reprint author]; Love, William [Reprint author]; Sampas, Nick [Reprint author]; Templin, Cathy [Reprint author]; Villanueva, Heidee [Reprint author]; Webb, Peter [Reprint author]; Westall, Mark [Reprint author]
CS Agilent Technologies, Palo Alto, CA, USA
SO International Genome Sequencing and Analysis Conference, (2000) Vol. 12, pp. 32. print.
Meeting Info.: 12th International Genome Sequencing and Analysis Conference. Miami Beach, Florida, USA. September 12-15, 2000.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 24 Oct 2001
Last Updated on STN: 23 Feb 2002
AB Angiogenesis is the process by which blood vessels form from either existing vessels or de novo and is critical to the normal development of the vasculature and the pathological progression of cancer, arthritis and numerous inflammatory diseases. We have used a proprietary ink jet deposition system to generate cDNA microarrays populated with cDNAs from subtracted libraries derived from endothelial cells induced to undergo angiogenesis in vitro. Experiments with these microarrays are expected to reveal genes that are endothelial cell specific, induced or suppressed during the angiogenic process and operative during angiogenesis in vivo. We have executed a series of control experiments in which identical samples are labeled with Cy3 and Cy5, "self:self experiments", in order to characterize the reproducibility, sensitivity, and reliability of expression ratio data from these arrays. We have designed algorithms for our data analysis package that allow us to measure the significance of specific gene expression ratios based on signal and background intensities as well as the results from the self:self experiments. We will present the results of angiogenic endothelial subtracted cDNA microarrays hybridized with in vitro and in vivo derived samples representing different stages of the angiogenic process.

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* * * * * * * * * *   Welcome to STN International   * * * * * * * * * *

 NEWS  1           Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2           "Ask CAS" for self-help around the clock
 NEWS  3  SEP 09   CA/CAplus records now contain indexing from 1907 to the
                   present
 NEWS  4  DEC 08   INPADOC: Legal Status data reloaded
 NEWS  5  SEP 29   DISSABS now available on STN
 NEWS  6  OCT 10   PCTFULL: Two new display fields added
 NEWS  7  OCT 21   BIOSIS file reloaded and enhanced
 NEWS  8  OCT 28   BIOSIS file segment of TOXCENTER reloaded and enhanced
 NEWS  9  NOV 24   MSDS-CCOHS file reloaded
 NEWS 10  DEC 08   CABA reloaded with left truncation
 NEWS 11  DEC 08   IMS file names changed
 NEWS 12  DEC 09   Experimental property data collected by CAS now available
                   in REGISTRY
 NEWS 13  DEC 09   STN Entry Date available for display in REGISTRY and CA/CAplus
 NEWS 14  DEC 17   DGENE: Two new display fields added
 NEWS 15  DEC 18   BIOTECHNO no longer updated
 NEWS 16  DEC 19   CROPU no longer updated; subscriber discount no longer
                   available
 NEWS 17  DEC 22   Additional INPI reactions and pre-1907 documents added to CAS
                   databases
 NEWS 18  DEC 22   IFIPAT/IFIUDB/IFICDB reloaded with new data and search fields
 NEWS 19  DEC 22   ABI-INFORM now available on STN

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               MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
               AND CURRENT DISCOVER FILE IS DATED 23 SEPTEMBER 2003
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 NEWS INTER    General Internet Information
 NEWS LOGIN    Welcome Banner and News Items
 NEWS PHONE    Direct Dial and Telecommunication Network Access to STN
 NEWS WWW      CAS World Wide Web Site (general information)

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=> file medline, biosis
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.21       0.21

FILE 'MEDLINE' ENTERED AT 16:35:53 ON 25 JAN 2004
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STN Columbus

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FILE 'BIOSIS' ENTERED AT 16:35:53 ON 25 JAN 2004
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=> s microarray and detritus
L1            0 MICROARRAY AND DETRITUS

=> search microarray and dirt
L2            0 MICROARRAY AND DIRT

=> search microarray and (noise removal)
L3            0 MICROARRAY AND (NOISE REMOVAL)

=> s microarray and noise
L4          176 MICROARRAY AND NOISE

=> s l4 and (removal or correction)
L5            5 L4 AND (REMOVAL OR CORRECTION)

=> duplicate remove l4
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
PROCESSING COMPLETED FOR L4
L6          120 DUPLICATE REMOVE L4 (56 DUPLICATES REMOVED)

=> duplicate remove l5
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
PROCESSING COMPLETED FOR L5
L7            3 DUPLICATE REMOVE L5 (2 DUPLICATES REMOVED)

=> d 1-3 bib ab
```

L7 ANSWER 1 OF 3 MEDLINE on STN
Full Text

AN 2002628313 IN-PROCESS
DN PubMed ID: 12385996
TI An automatic block and spot indexing with k-nearest neighbors graph for **microarray** image analysis.
AU Jung Ho-Youl; Cho Hwan-Gue
CS Department of Computer Science, Pusan National University, San-30, Jangjeon-dong, Keumjeong-gu, Pusan, 609-735, Korea.
SO Bioinformatics (Oxford, England), (2002 Oct) 18 Suppl 2 S141-51. Journal code: 9808944. ISSN: 1367-4803.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-DATA-REVIEW; IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20021019
Last Updated on STN: 20021213
AB Motivation: In this paper, we propose a fully automatic block and spot indexing algorithm for **microarray** image analysis. A **microarray** is a device which enables a parallel experiment of ten to hundreds of thousands of test genes in order to measure gene expression. Due to this huge size of experimental data, automated image analysis is gaining importance in **microarray** image processing systems. Currently, most of the automated **microarray** image processing systems require manual block indexing and, in some cases, spot indexing. If the **microarray** image is large and contains a lot of **noise**, it is very troublesome work. In this paper, we show it is possible to locate the addresses of blocks and spots by applying the Nearest Neighbors Graph Model. Also, we propose an analytic

model for the feasibility of block addressing. Our analytic model is validated by a large body of experimental results. Results: We demonstrate the features of automatic block detection, automatic spot addressing, and **correction** of the distortion and skewedness of each **microarray** image. Contact: hyjung@pearl.cs.pusan.ac.kr

L7 ANSWER 2 OF 3 MEDLINE on STN DUPLICATE 1
Full Text
AN 2002733483 IN-PROCESS
DN PubMed ID: 12047881
TI Statistical intelligence: effective analysis of high-density **microarray** data.
AU Draghici Sorin
CS 431 State Hall, Dept of Computer Science, Wayne State University, 48202, tel: +1 313 577 5484; fax: +1 313 577 6868, Detroit, MI, USA.
SO Drug discovery today, (2002 Jun 1) 7 (11 Suppl) S55-63.
Journal code: 9604391. ISSN: 1359-6446.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-DATA-REVIEW; IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20021227
Last Updated on STN: 20031217
AB **Microarrays** enable researchers to interrogate thousands of genes simultaneously. A crucial step in data analysis is the selection of subsets of interesting genes from the initial set of genes. In many cases, especially when comparing genes expressed in a specific condition to a reference condition, the genes of interest are those which are differentially regulated. This review focusses on the methods currently available for the selection of such genes. Fold change, unusual ratio, univariate testing with **correction** for multiple experiments, ANOVA and **noise** sampling methods are reviewed and compared.

L7 ANSWER 3 OF 3 MEDLINE on STN DUPLICATE 2
Full Text
AN 2001009198 MEDLINE
DN 20472457 PubMed ID: 11017932
TI Evaluation of the performance of a p53 sequencing **microarray** chip using 140 previously sequenced bladder tumor samples.
CM Comment in: Clin Chem. 2000 Oct;46(10):1523-5
AU Wikman F P; Lu M L; Thykjaer T; Olesen S H; Andersen L D; Cordon-Cardo C; Orntoft T F
CS Molecular Diagnostic Laboratory, Department of Clinical Biochemistry, Aarhus University Hospital, 8200 Aarhus N, Denmark.
SO CLINICAL CHEMISTRY, (2000 Oct) 46 (10) 1555-61.
Journal code: 9421549. ISSN: 0009-9147.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200010
ED Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001025
AB BACKGROUND: Testing for mutations of the TP53 gene in tumors is a valuable predictor for disease outcome in certain cancers, but the time and cost of conventional sequencing limit its use. The present study compares traditional sequencing with the much faster **microarray** sequencing on a commercially available chip and describes a method to increase the specificity of the chip. METHODS: DNA from 140 human bladder tumors was

extracted and subjected to a multiplex-PCR before loading onto the p53 GeneChip from Affymetrix. The same samples were previously sequenced by manual dideoxy sequencing. In addition, two cell lines with two different homozygous mutations at the TP53 gene locus were analyzed. RESULTS: Of 1464 gene chip positions, each of which corresponded to an analyzed nucleotide in the sequence, 251 had background signals that were not attributable to mutations, causing the specificity of mutation calling without mathematical **correction** to be low. This problem was solved by regarding each chip position as a separate entity with its own **noise** and threshold characteristics. The use of background plus 2 SD as the cutoff improved the specificity from 0.34 to 0.86 at the cost of a reduced sensitivity, from 0.92 to 0.84, leading to a much better concordance (92%) with results obtained by traditional sequencing. The chip method detected as little as 1% mutated DNA. CONCLUSIONS: **Microarray**-based sequencing is a novel option to assess TP53 mutations, representing a fast and inexpensive method compared with conventional sequencing.

=> log y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	5.96	6.17

STN INTERNATIONAL LOGOFF AT 16:41:18 ON 25 JAN 2004